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Fig. 1

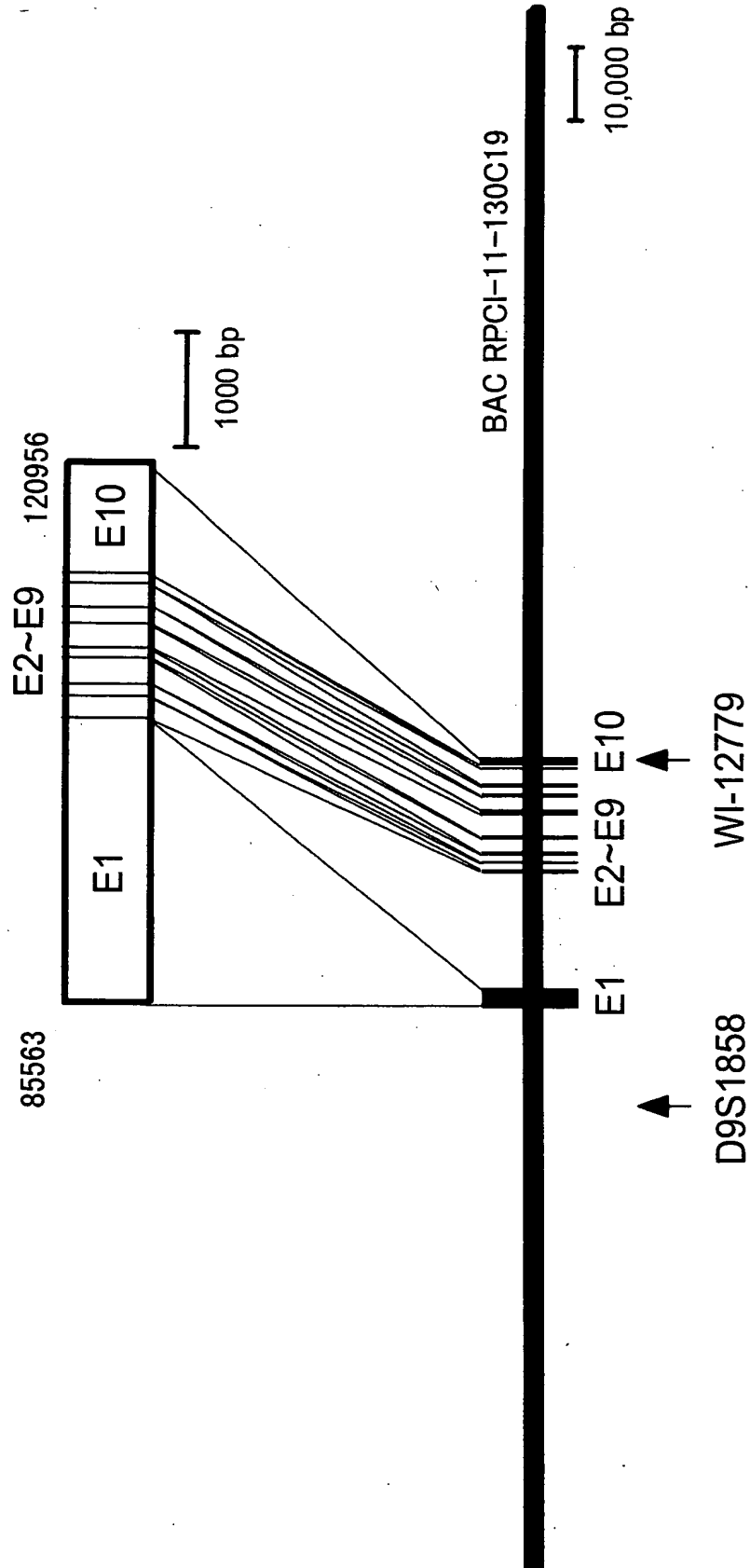
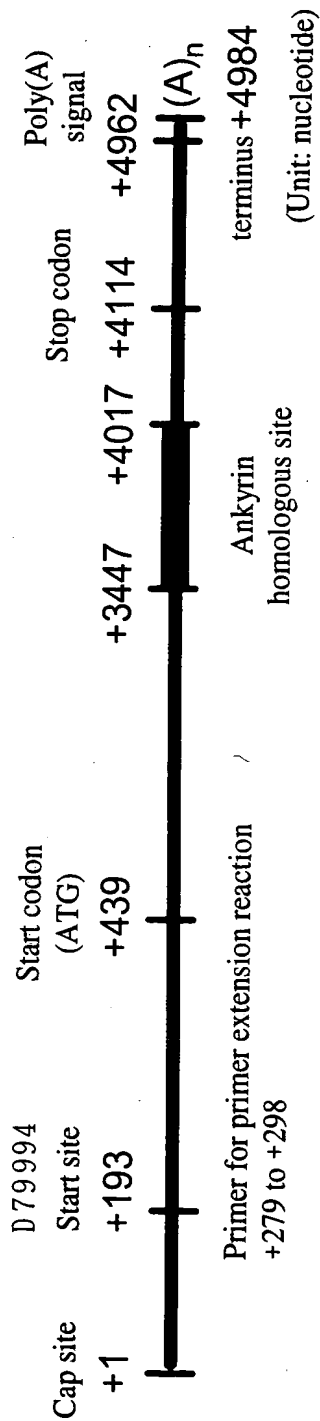
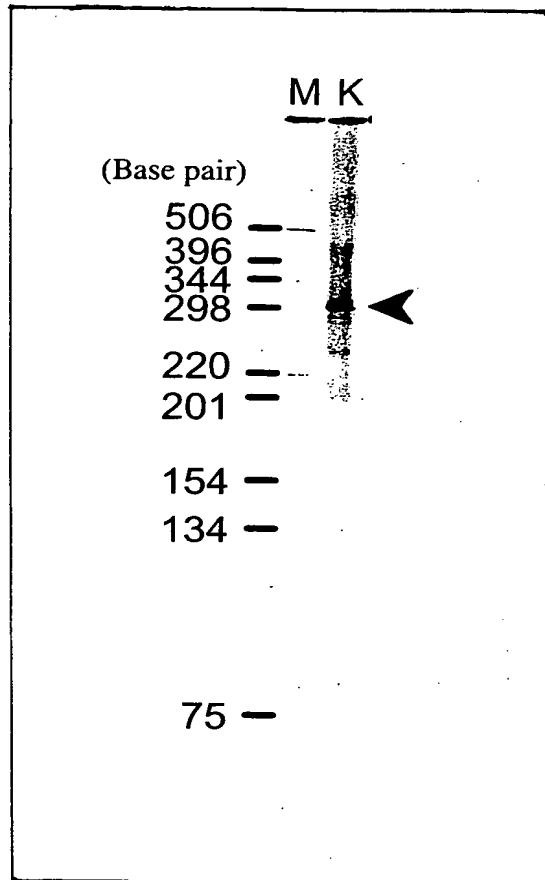


Fig. 2A



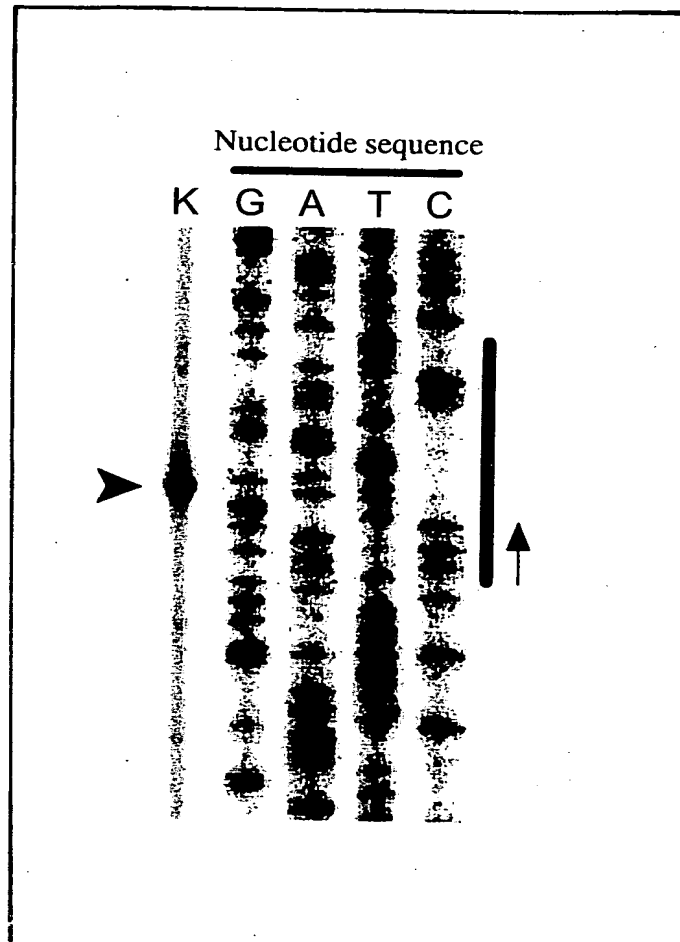
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Fig. 2B



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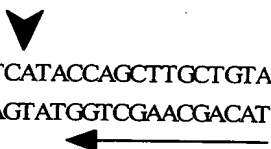
Fig. 2C



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Fig. 2D

AAAACATAGGTGTGTCAACTCTTAAAATCATACCAGCTTGCTGTA
TTTTGTATCCACACAGTTGAGAATTTTAGTATGGTCGAACGACAT



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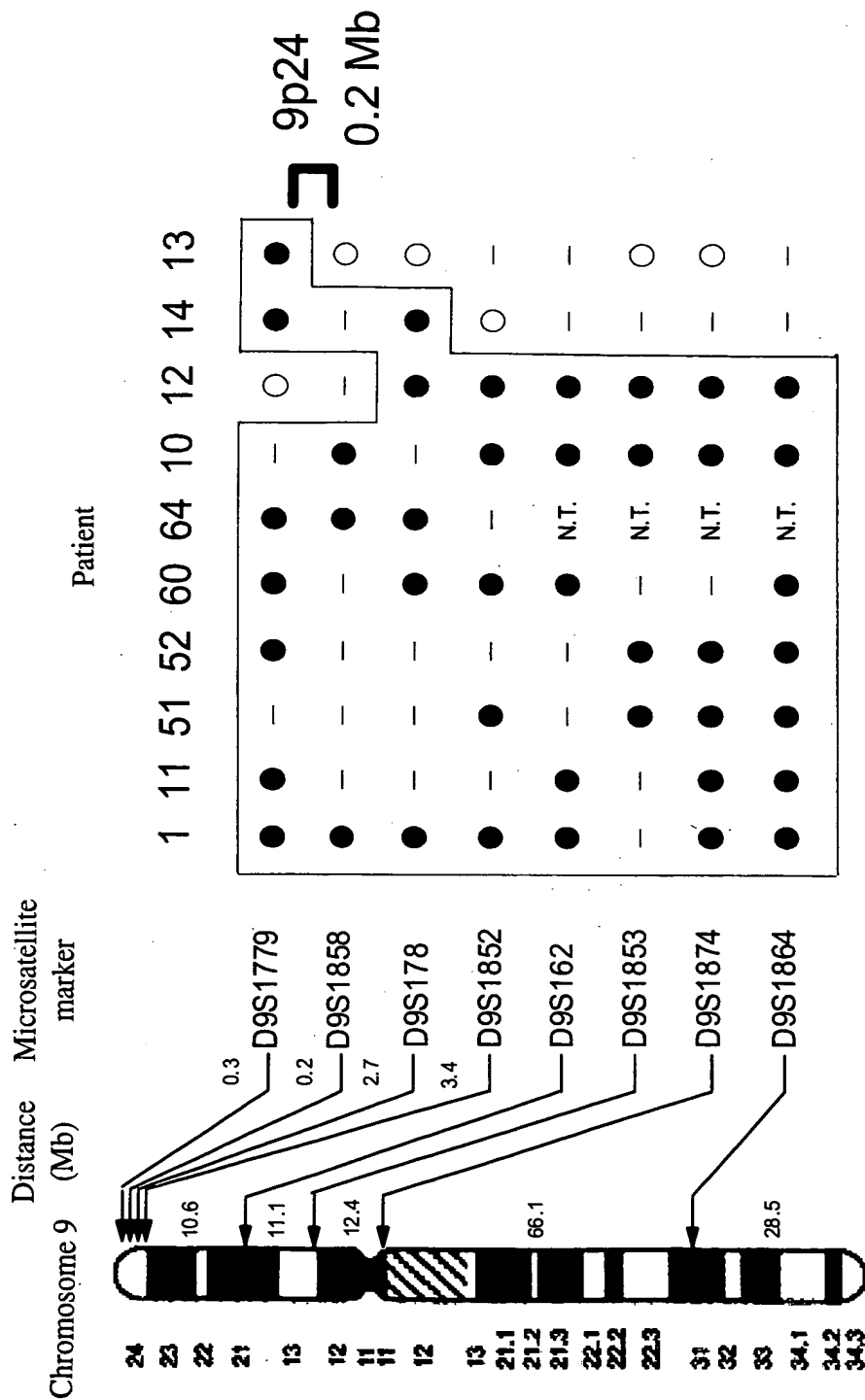
Fig. 3

METRRRLERATMQMTPEFRPRRLASFGGMGTSSLPFVSGNHNPAKHQLONGYQ
GNGDYGSAAPAPTSSMGSSIRHSPSSGISTPTNVSPMHLQHIREQMAIALKRLKE
LEEQVRTIPVLQKISVLQEEKRLVSQLKNQRAASQINVCGRKRSYSAGNASQLEQL
SRARRSGGELYIDYEEEEEMETVEQSTQRIKEFRQLTADMQALEQKIQDSSCEASSELR
NGECRSVAVGAEEENMNDIVVYHRGSRCKDAAGTIVEMRNCVSVTEAMLGVMTEADK
EIELQQQTIEALKEKIYRLEVQLRETHDREMTKLKQELQAAGSRKKVDKATMAQPLVF
SKVVEAVVQTRDQWVGSHMDLVDTCVGTSVETNSVGISQCECKNKVVGPELPMNWWIV
KERVEMHDCAGRSVEMCDKSVSVESVCETGNTSESVNDLTLLKTNLNLKEVRSIGC
GDCSVDVTVCSPKECASRGVNTAEVSVQVEAAVMVPTADQDSTDLQVHQFTNTETA
TLIESCTNTCLSTLDKQSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGF
DRPSAVTKESGVGININDNYLVGLKMRTIACGPPQLTVGLTASRRSVGVGDDDPVGES
LENPQPAPLGMMTGLDHYIERIQKLLAEQQTLAENYSELAEAFGEPHSQMSGSLNSQL
ISTLSSINSVMKSASTEELRNPDFQKTSGLKITGNLYGTCCKGGLQSGSPSSQTSQP
EQEVGTSEGKPISSLDAPFTQEGTLPVNLTDQIAAGLYACTNNESTLKSIMKKDGN
KDSNGAKKNLQFVINGGVETTSSDDSSDESSSESDECDVIEYPLEEEEEEEDEDT
RGMAEGHHAVNIEGLKSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND
PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAISPDVLRVYINLADGN
GN

Ankyrin homologous site
1006-1162

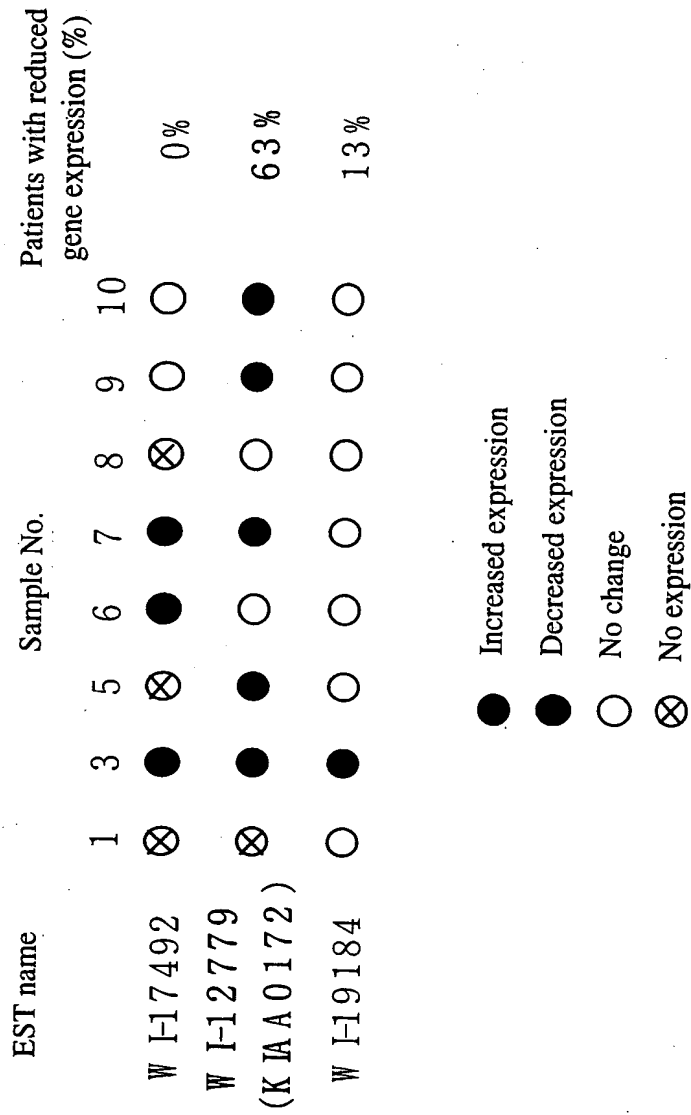
TALHYSVSHSNFEIVKLLLDADVNCVDHQNKAGTPIMLAALAAVEAEKDMRIVEELFG
CGDVNAKASQAGQTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHGHVE
IVKLLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLL
YAHVNFKAQSPGTPRLGRKTSPPGTHRGSFD

Fig. 4



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Fig. 5



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Fig. 6

| Codon No. | D79994 | Mutation | Change in amino acid | Patient No. | Frequency (%) |
|-----------|--------------------------|----------|----------------------|-------------------------------|---------------|
| 52 | CAC | CAG | His→Gln | 56 | 1/75 (1.3) |
| 168 | GCG | GTG | Ala→Val | 4 | 1/75 (1.3) |
| 268-269 | (6 nucleotides inserted) | +GCTGTA | (Ala-Val) Inserted | 64 | 1/75 (1.3) |
| 269 | GTA | GGA | Val→Gly | 90 | 1/75 (1.3) |
| 274 | GAG | CAG | Glu→Gln | 8, 23, 49, 52, 87, 90, 92 | 7/75 (9.3) |
| 306 | TCC | GCC | Ser→Ala | 4, 22, 68, 84, 86 | 5/75 (6.7) |
| 506 | GCA | GTA | Ala→Val | 15, 83 | 2/75 (2.6) |
| 509 | CGT | CAT | Arg→His | 4, 22, 41, 48, 51, 68, 84, 86 | 8/75 (10.6) |
| Total | | | | 19/75 | (25.3) |

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Fig. 7

| Codon No. | Amino acid | GenBank Data | SNP | Patient No. | Frequency (%) |
|-----------|------------|--------------|-----|---|---------------|
| 273 | Val | GTT | GTG | 11 | 1.3 |
| 299 | Leu | CTG | CTC | 4, 22, 51, 64, 60, 11, 66, 16, 17, 19 | 13.3 |
| 372 | His | CAC | TAC | 64 | 1.3 |
| 380 | Val | GTT | GTG | 42 | 1.3 |
| 497 | Val | GTT | GTG | 51 | 3.5 |
| 453 | Asn | AAC | AAT | 16, 21, 52, 8, 23, 41, 49, 51, 67, 68, 84, 86, 89, 91 | 18.6 |
| 478 | Asp | GAC | GAT | 4, 22, 41, 48, 51, 68, 84, 86 | 10.7 |
| 507 | Val | GTG | GTT | 66, 16 | 2.6 |
| 1003 | Asn | AAC | AAT | 10 | 1.3 |
| 1120 | Gly | GGG | GCC | 12 | 1.3 |

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Fig. 8

| Patient No. | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | |
|-------------|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|--|
| LOH | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | |
| D9S1779 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | |
| D9S1858 | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | |
| Mutation | | | | | | | | | | | | | | | | | | | | | | | | |
| SNP | | | | | | | | | | | | | | | | | | | | | | | | |

○ : No LOH
● : LOH
● : Mutation positive
● : SNP positive

| Patient No. | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 |
|-------------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| LOH | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| D9S1779 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| D9S1858 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| Mutation | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● |
| SNP | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● |

| Patient No. | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | Frequency |
|-------------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|---------------|
| LOH | | | | | | | | | | | | | | | | | | | | | | | | | | | 6/49 (27.3%) |
| D9S1779 | | | | | | | | | | | | | | | | | | | | | | | | | | | 4/49 (14.3%) |
| D9S1858 | | | | | | | | | | | | | | | | | | | | | | | | | | | 19/75 (25.3%) |
| Mutation | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | 26/75 (34.7%) |
| SNP | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | ● | |

Fig. 9

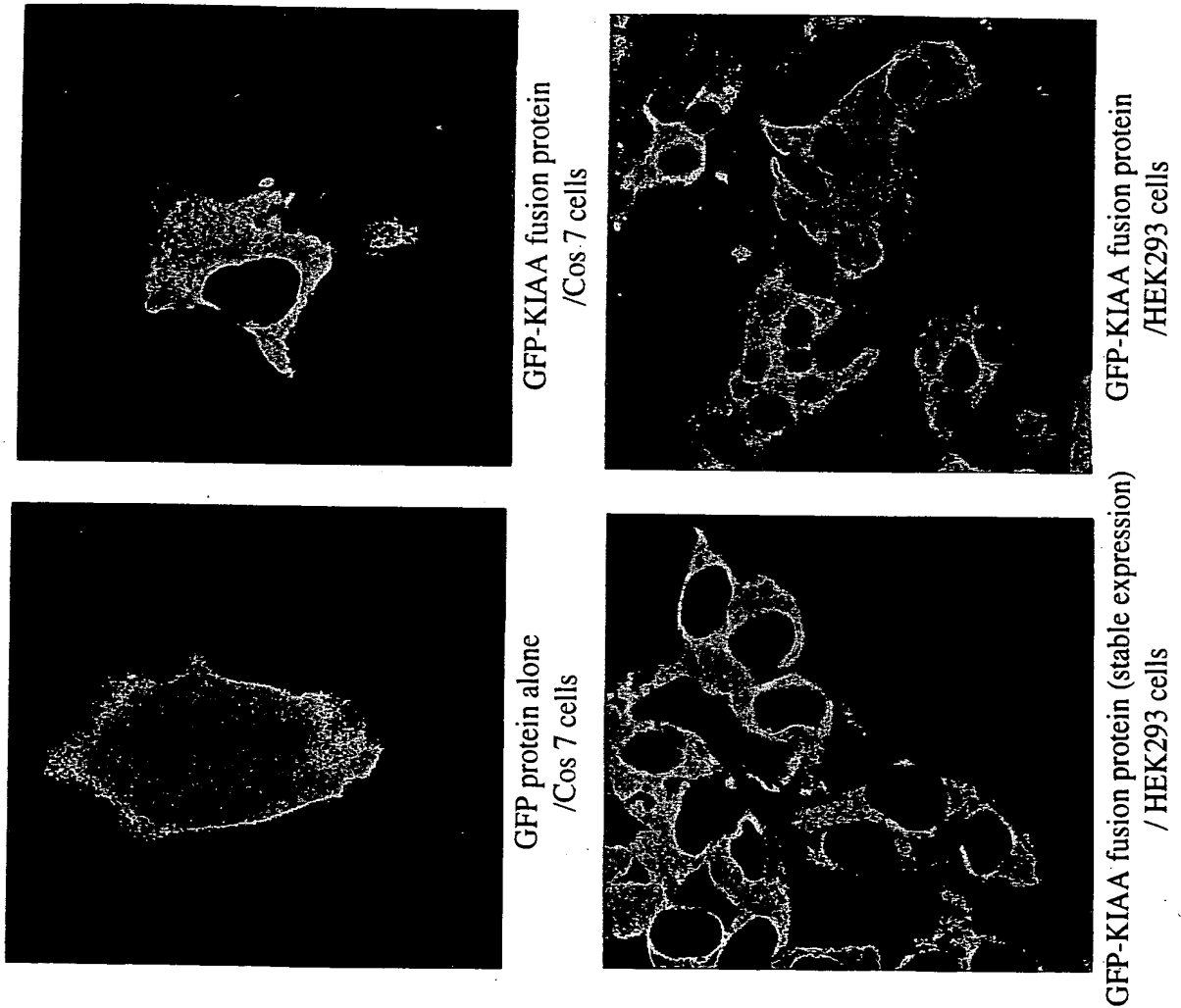
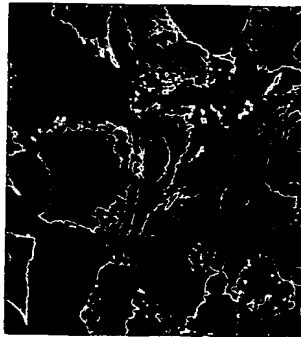


Fig. 10A

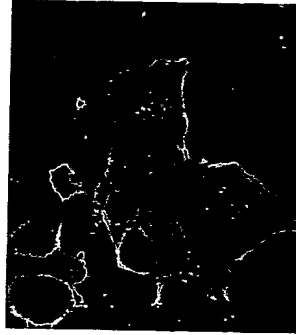
Results of immunostaining using an anti-KIAA0172 antibody



Results of staining of
VMRC-RCW cells



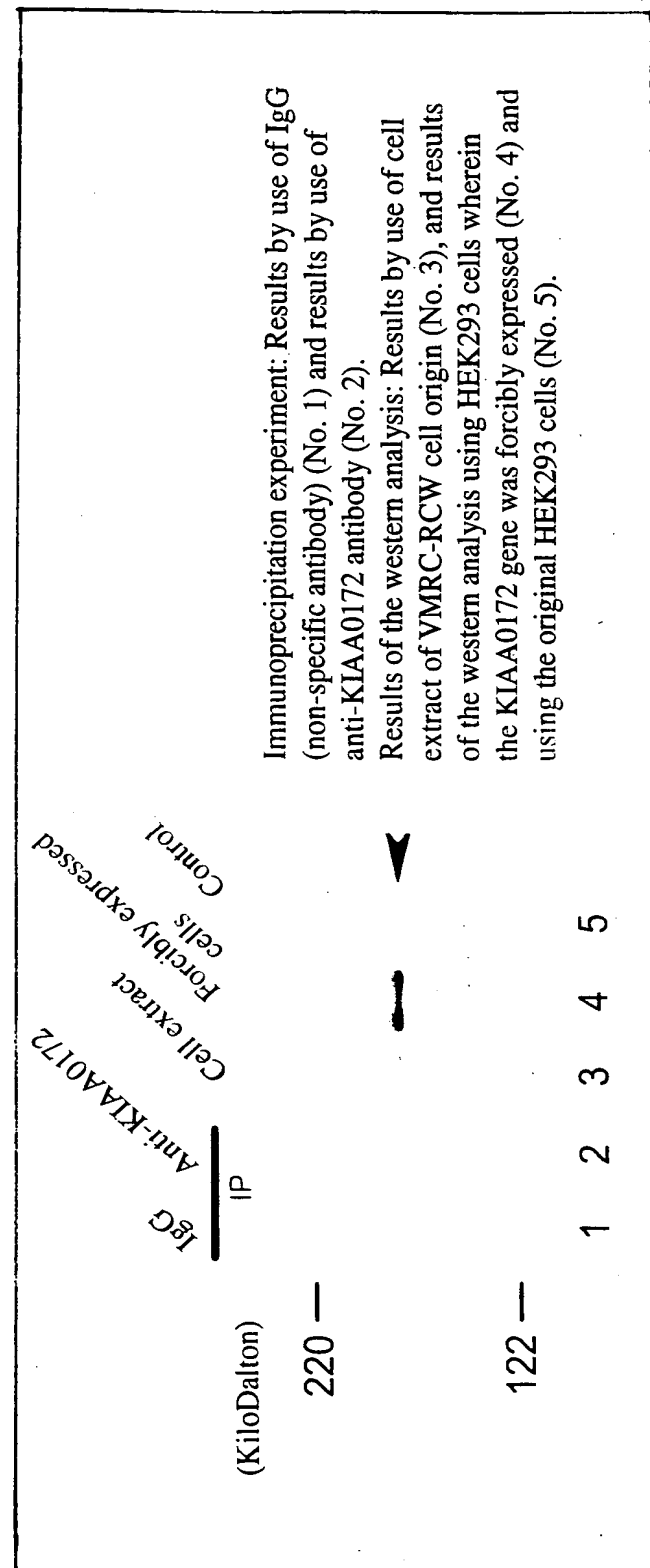
Results of staining of
VMRC-RCW cells
with the antigen added



Results of staining of
HEK293 cells in which KIAA0172
gene was forcibly expressed

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Fig. 10B



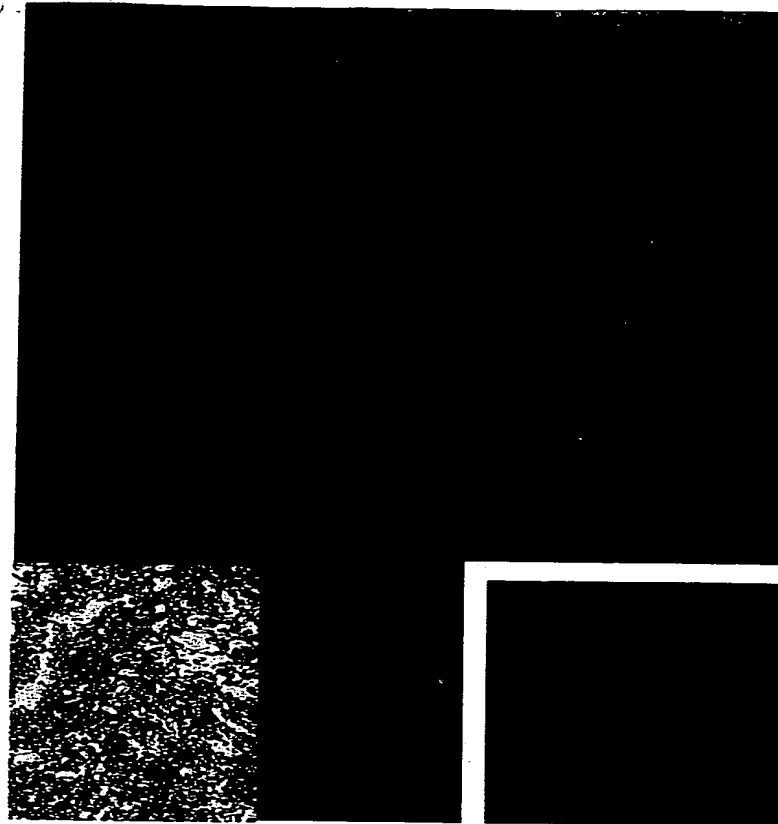
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Fig. 11

Normal tissue



Cancer tissue



Upper left shows the result of HE staining and
lower left is an enlarged view, respectively

Fig. 12A

Result of allele loss in the cancer tissue DNA in gene scan analysis

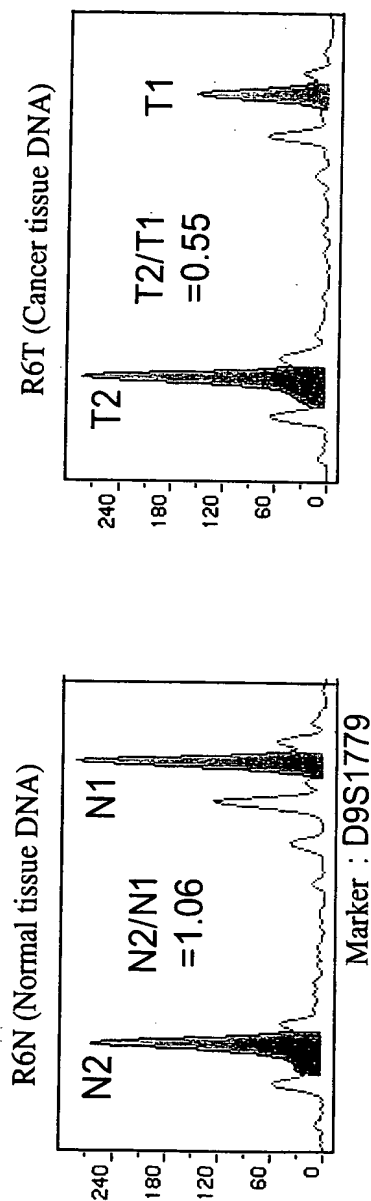


Fig. 12B

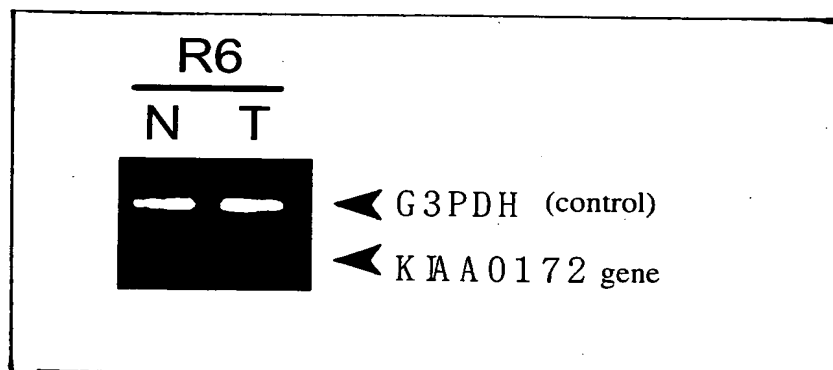
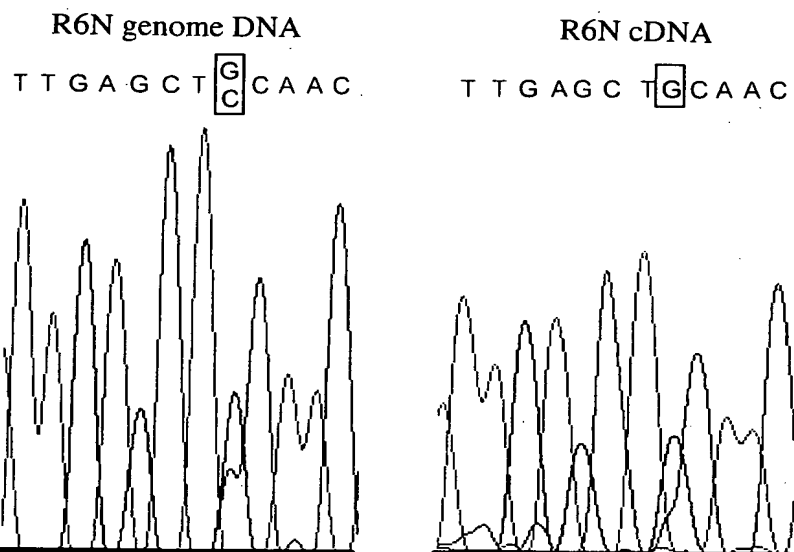


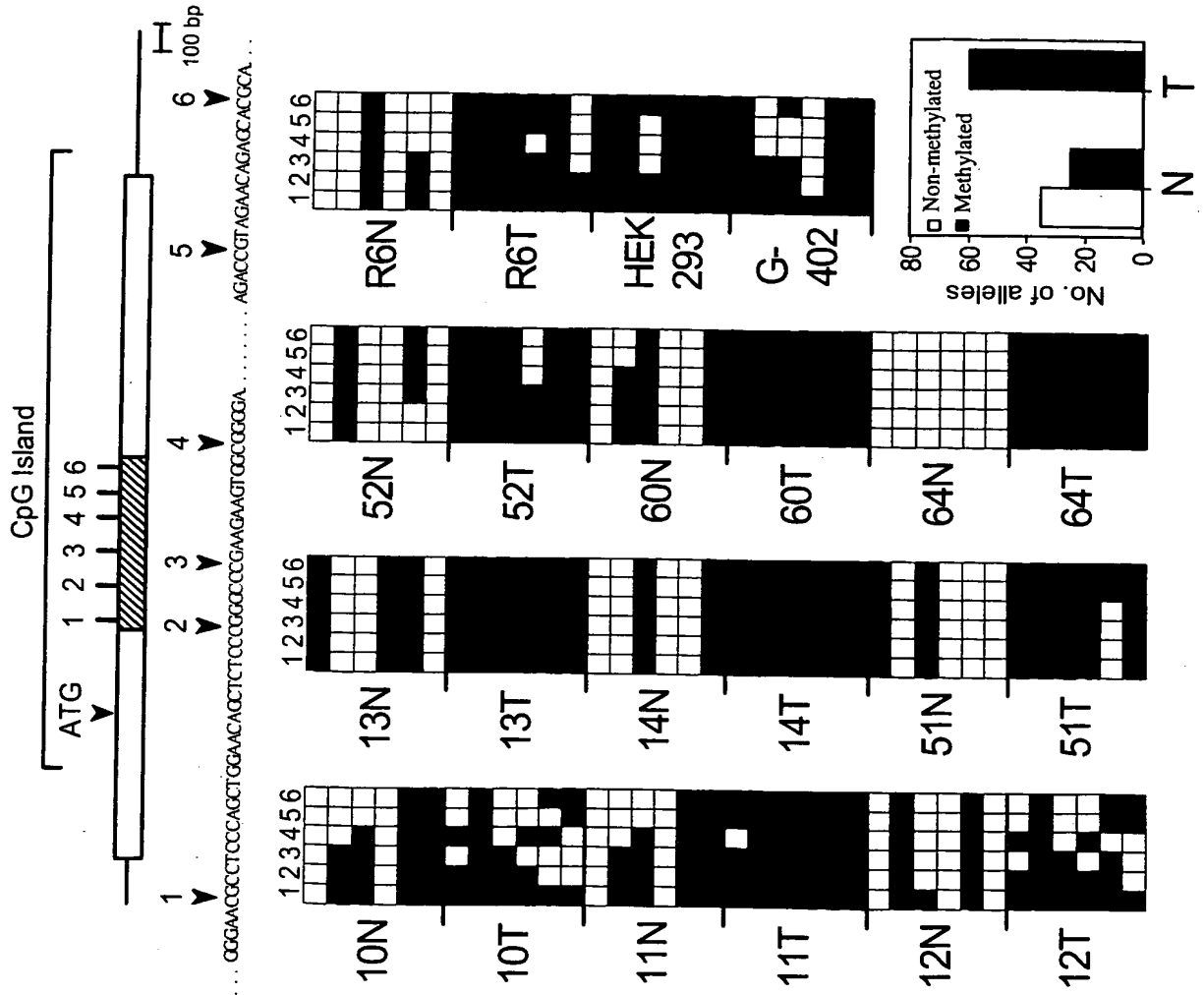
Fig. 12C

Result of allele-specific expression using single nucleotide polymorphism



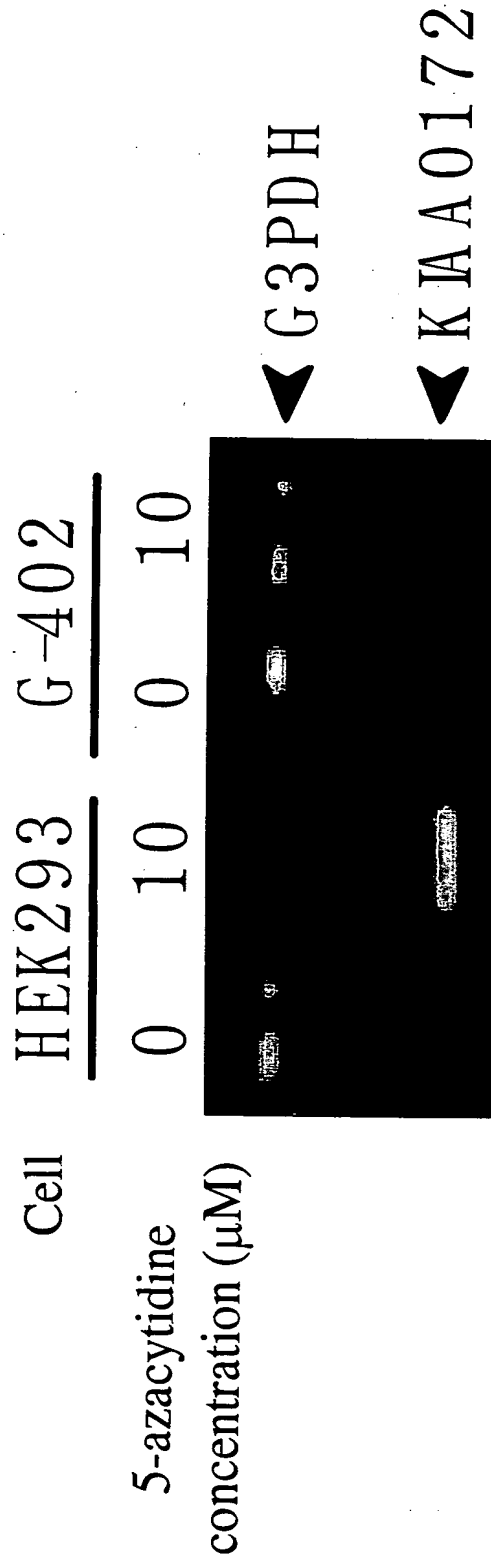
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Fig. 13



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Fig. 14



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Fig. 15A

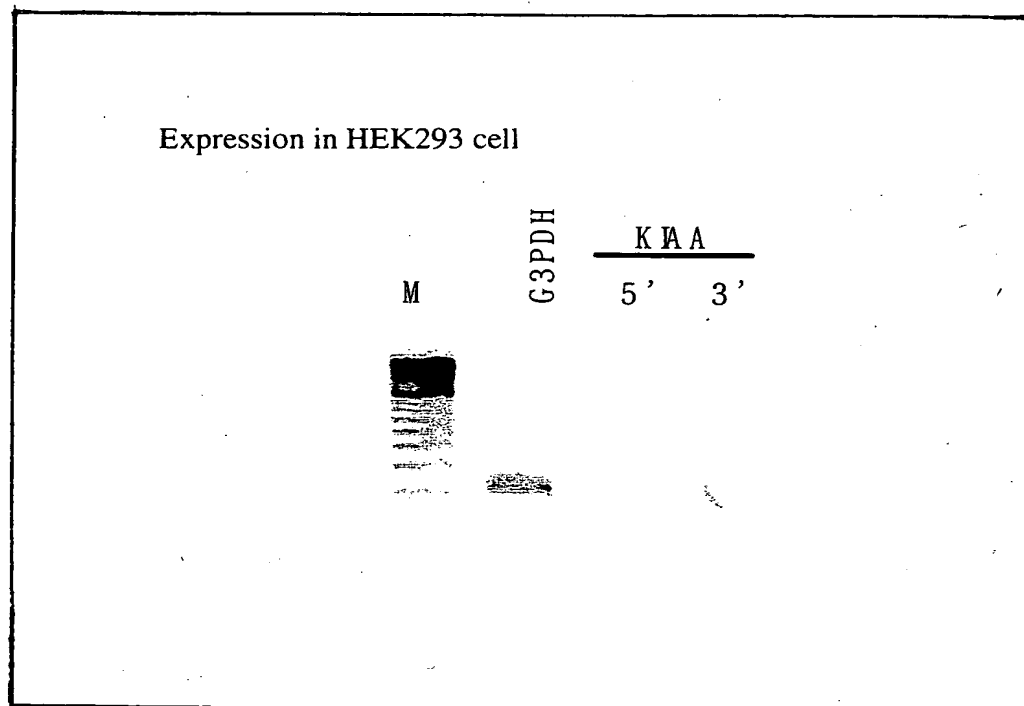
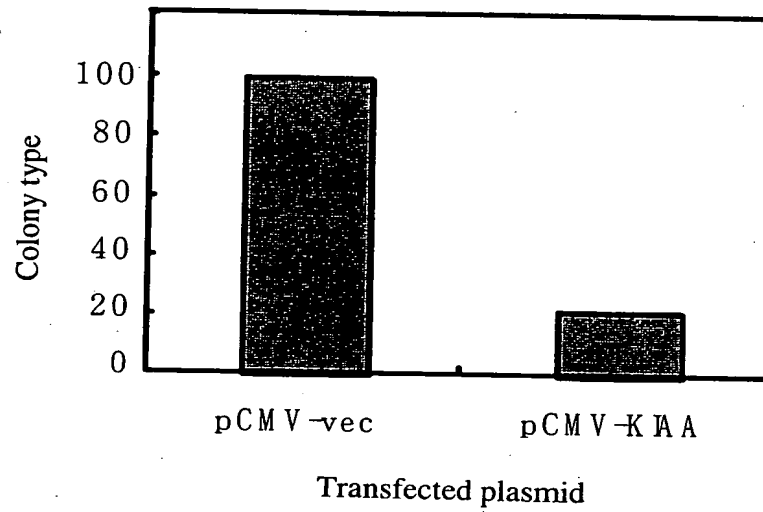


Fig. 15B

Cell proliferation suppressing ability when transfected into HEK293 cell



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Fig. 16A

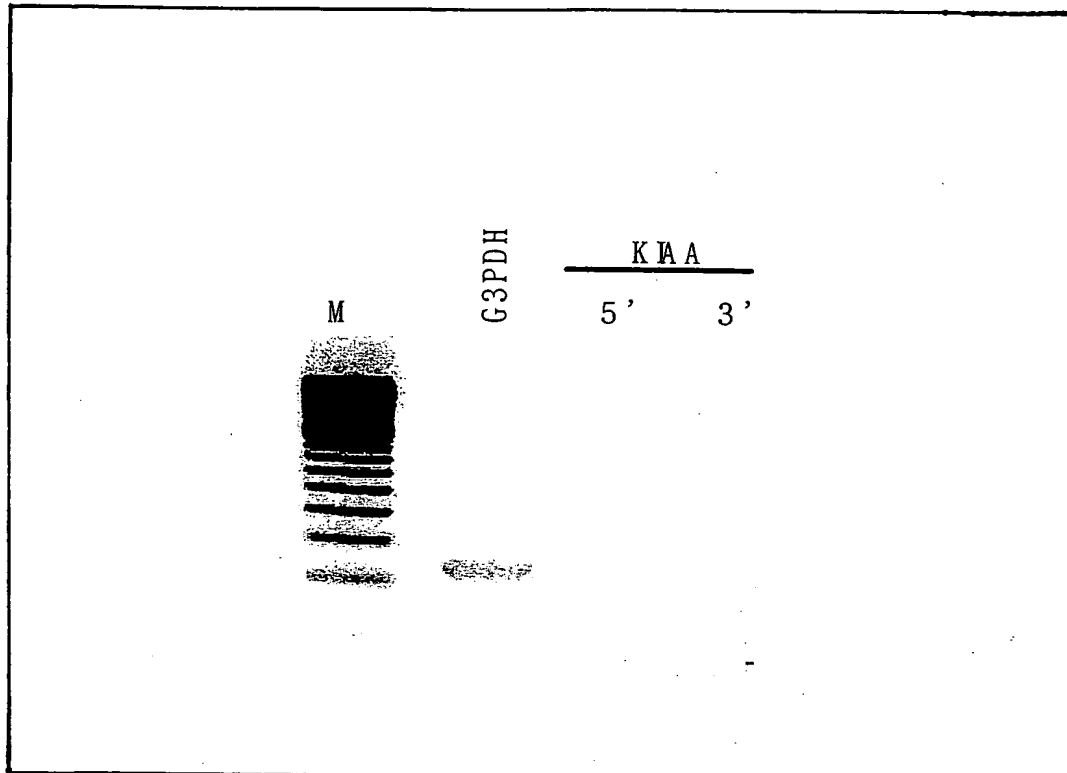
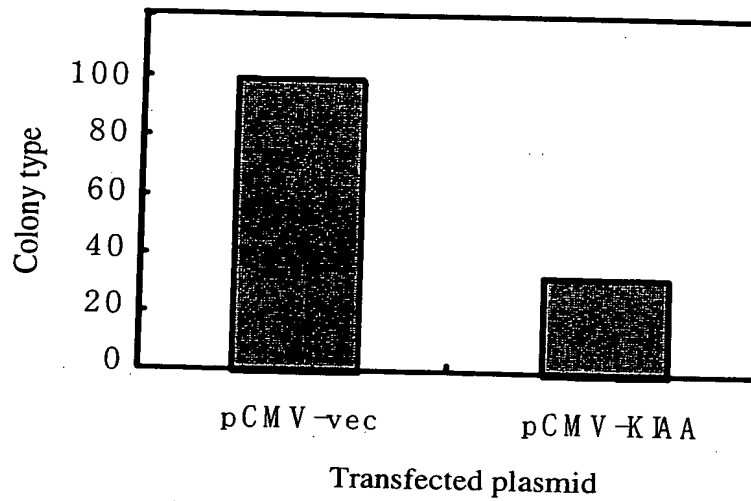


Fig. 16B

Cell proliferation suppressing ability when transfected into G-402 cell



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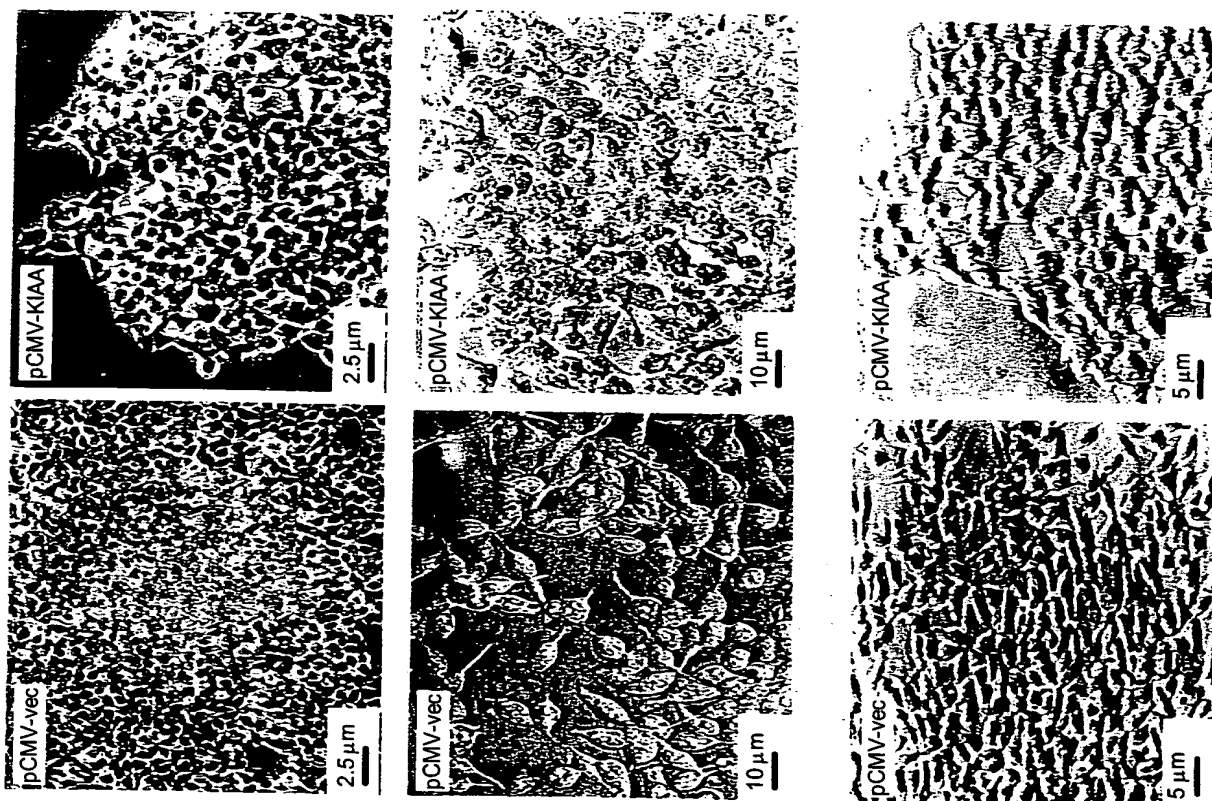
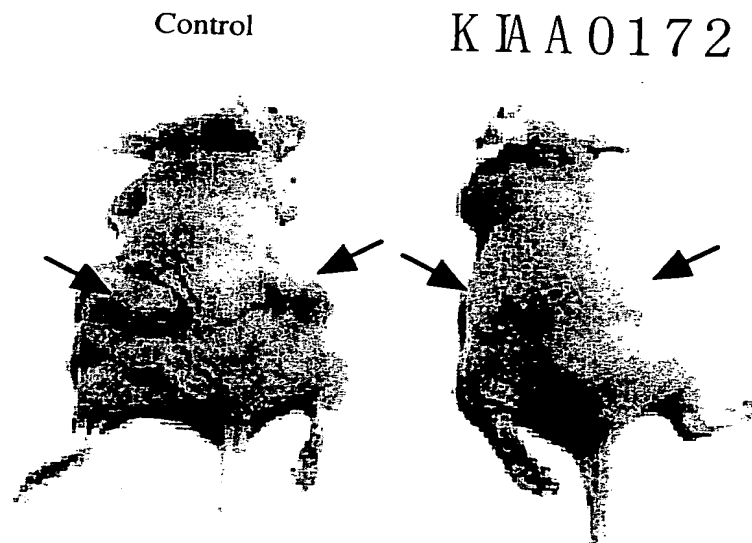


Fig. 17

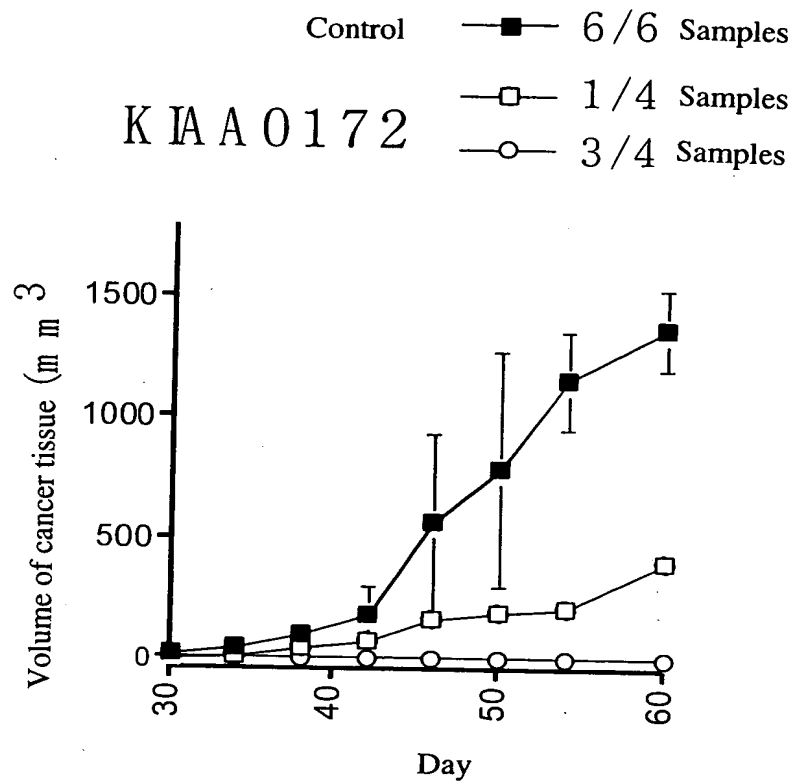
Fig. 18A

Results of experiments where HEK293 cells expressing vector (control) and HEK293 cells expressing KIAA0172 gene were transplanted into abdominal cavity, respectively



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Fig. 18B



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